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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yue, H., Tang, Y.T., Reddy, R., Yang, J., Patterson, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgCysLeuHisSerGluLysAlaHisAspLeuGlyIleThrCysCysAspPheSerSer
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              GlyIlePheLysMetAsnAsnIleAspGlyLysGluLeuLeuAsnLeuThrLysGluSer
                                                   GATTGGTCAGAGGAGGATGTCTCAACATGGCTTTGTGCACAAGATTTAAAAAGATCTTGTT
                                                                                                         GACCTGGAAACACTTTGCCAAGCAAGGAGCACAGAACATCAGCTGAAGCAATTTACCGAA
                                                                                                                                                                                                                                                                                                                             TATAAAAGTACACTGAGTGGGCACTGTGCTCCTGTTCTGGCTTGTGCTTTTTCCCATGAT 357
                                                                                                                                                                                                                                                                                                                                                                                   GATTGCCAAGTCAAAATTTGGATTGTTTCTTTTACCCATATCTTAGGTTTTGAATTAAAA
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AspTrpSerGluGluValValSerThrTrpLeuCysAlaGlnAspLeuLysAspLeuVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
/mol_type="unassigned DN/db_xref="taxon:9606"
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                                                                                                                      -----AlaArgArgThrGluHisGlnLeuLysGlnPheThrGlu 238
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Submitted (03-FEB-199) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

E glaren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Coste, P., Dehrellano, K., Depayre, E., Devon, K., Dewar, K., Cooke, P., Dehrellano, K., Depayre, E., Devon, K., Dewar, K., Cooke, P., Dehrellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehozaky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 147021)

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3 birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,

Baker,J., Baldwin,J., Barna,N., Beckerly,R., Benn,J., Brown,A.,

Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,

Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,

Cooke,P., DeArellano,K., Depayre,E., Dewon,K., Dewar,K.,

Donelan,L., Doyle,M., Ferreira,P., FrizHugh,W., Forrest,C.,

Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,

Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G.,

Karatas,A., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,

Karatas,A., Lehoczky,J., Lieu,C., Locke,K., Macdonald,P.,

Marquis,N., McSwan,P., McGurk,A., McKernan,K., McLaughlin,J.,

Marquis,N., Molla,M., Morris,W., Morrow,J., Mychaleckyj,J.,

Maylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,

Naylor,J., Niloff,M., O'Connor,T., O'Donnell,P., Pavlin,B.,

Peterson,K., Pollara, V., Riley,R., Roberts,D., Roy,A., Savery,P.,

Stange-Thomann,N., Stojanovic,N., Stone,C., Subramanian,A.,

Tesfaye,S., Torruella-Miller,I., Vassiliev,H., Vo,A., Wagner,A.,

Wheeler,J., Wu,X., Wyman,D., Ye,W.J. and Zody,M.
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Complement (6014860393)  /rpt_family="Alusq"  No.:  No.:  7.21e-55  Length: 147021  147021  15 Similarity: 55.06% Conservative: 36  Matches: 98 Match: 95 Match: 95 Match: 176  Conservative: 36  Match: 95 Match: 176  Conservative: 36  Mother: 176  Conservative: 376  Conservative: 376  Conservative: 376  Conservative: 376  Conservative: 376  Conservative: 376  Conserva	/rpt_family="AluSq"  ment Scores:  No.:  7.21e-55  Length: No.:  7.31e-55  Length: 147021  it Similarity: 55.06% Conservative: 36  Match: 35.81% Indels: 75  Gaps:  077-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 21 SerPheSerLeuLalaThrCysGarIGACGATGTCAACTGCTGTGCCTTC 106514  21 SerPheSerLeuLalaThrCysGarIGACGATGTCAACTGCTGTGCCTTC 106514	repeat_region
Complement (6014860393)  /**Pt_family="AluSq"**  nent Scores:  No.:  7.21e-55 Length: 147021  14 Similarity: 733.00 Matches: 176 Conservative: 36 Match: 35.81* Mismatches: 98 Match: 75 Mismatches: 75 Mismatches: 98  104-11-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaphe 20 106573 ATGGTGAAACTGATTCACACATTAGCTGATCATGGTGAACTGCTGTGCCTTC 106514  21 SerPheSerLeuLeuAlathiaThrCysSerLeuAspLysThrIleArgIntercers  1	/rpt_family="AluSq"  ment Scores:  No.:  17.21e-55  Length:  147021  it Similarity:  55.06%  Conservative:  36.061 Similarity:  45.71%  Mismatches:  98  Match:  98  Match:  176  Conservative:  98  Mismatches:  98  Mismatches:  98  777-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsmCysCysAlaPhe  106573 ATGGTGAAACTGATTCACACATTAGCTGATCATGGTGAACTGCTGTGCCTTC  106573 ATGGTGAAACTGATTCACACATTAGCTGATCATGGTGAACTGCTGTGCCTTC  106573 ATGGTGAAACTGATCACACATTAGCTGATCATGGTGAACTGCTGTGCCTTC  106574  21 SerPheSerLeuLehAlaThrCysSerLeuAspLysThrI]eArgInsTysCysSerLeuAspLysThrII]eArgInsTysCysSerLeuAspLysThrII]eArgInsTysCysSerLeuAspLysThrII]eArgInsTysCysSerLeuAspLysThrII]eArgInsTysCysSerLeuAspLysThrII]eArgInsTysCysSerLeuAspLysThrII]eArgInsTysCysSerLeuAspLysThrII]eArgInsTysCysSerLeuAspLysThr	repeat_region
Complement (6014860393)  /rpt_family="Alusq"  No.:  No.:  7.21e-55  Length: 147021  It Similarity: 45.71% Matches: 36  Conservative: 36  Match: 35.81%  Mismatches: 98  Match: 95  Match: 35.81%  Mismatches: 98  Match: 95  Match: 176  Conservative: 36  Mismatches: 98  Match: 176  O77-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeulleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20  106573 ATGGTGAAACTCATTACCACATTAGCTGATCATCGTGAACGATGTCAACTGCTGTGCCTTC 106514  21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrLieArgJeuTyrSerLeuArg 40  O77-111-11	/rpt_family="Alusq"  nent Scores:  NO.:  7.21e-55  Length: 147021  16 Similarity: 55.06% Conservative: 36 Conservative: 36 Match: 95 Match: 96 Mat	repeat_region
Complement (6014860393)  /rpt_family="Alusq"  No.:  No.:  7.21e-55  Length: 147021  147021  147021  Length: 147021  Length: 156  Conservative: 36  Matches: 98  Match: 95  Match: 96  Matches: 96  Matc	/rpt_family="AluSq"  ment Scores:  No.:  147021  ment Scores:  7.21e-55  Length: 147021  it Similarity: 55.06% Conservative: 36  Match: 35.81% Indels: 75  Gaps:  077-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeulleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20  106573 ATGGTGAAACTGATTCACACATTAGCTGATCATGGTGACGATGTCAACTGCTGTGCCTTC 21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrlleArgLeuTyrSerLeuArg 40  106513 TCCTTTTTCCTH\[	repeat_region
Complement (6014860393)  /**Fpt_family="AluSq"  ment Scores:  No.:  7.21e-55  Length:  147021  It Similarity: 55.06%  Conservative: 36  Local Similarity: 45.71%  Mismatches: 98  Indels: 75  Gaps: 11  077-111-13 (1-384) x AC006501 (1-147021)  MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaphe 20  106573 ATGGTGAAACTGATCACACATTAGCTGATCATGGTGAACTGGTGACCTTTCCCTTTC 106514	Complement (60148	repeat_region
Complement (6014860393)  /**FPt_family="Alusq"	/rpt_family="Alusq"  nent Scores:  No.:  7.21e-55  Length:  733.00  Matches:  745.71  Mismatches:  9  Gaps:  11  077-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20  106573 ATGGTGAAACTGATTCACACATTAGCTGATCATGGTGAACTGCTGTGCCTTC 106514  21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40  106513 TCCTTTTCCCTCTTGGCTACTTGCTCCTTGGAAAACAAATCAAATCAATTTCCCTTTGGAAACAAATCACCTTTTTT	repeat_region
Complement (6014860393)  /*pt_family="Alusq"  No.:  No.:  7.21e-55  Length: 147021  Resident Scores:  7.21e-55  Length: 176  Conservative: 36  Matches: 98  Match: 98  Match: 95  Match: 95  Match: 95  Match: 95  Match: 95  Match: 176  Conservative: 36  Match: 95  Match: 95  Match: 95  Match: 176  Conservative: 36  Match: 95  Match: 95  Match: 95  Match: 95  Match: 95  Match: 95  Match: 176  Conservative: 36  Match: 95  Match: 96  Matches: 96	/rpt_family="AluSq"  ment Scores:  No.:  7.21e-55  Length: No.:  7.31e-55  Length: 147021  it Similarity: 55.06% Conservative: 36  Matches: 98  Match: 98  Match: 156  O77-111-13 (1-384) x AC006501 (1-147021)  1 MetVallysLeulleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20  106573 ATGGTGAAACTGATTCACACATTAGCTGACAACAACGATGTCACTGTGCCTTC 106514  21 SerPheSerLeuLalaThrCysSerLeuAspLysThrleArgLeuTyrSerLeuArg 40  106513 TCCTTTTCCCTCTTGGCTACTTGCTCCTTGGACAAAACAATTCGCCTTGTACTGTTACGTACG	repeat_region
Complement (6014860393)	Complement (60148)	repeat_region
Complement (6014860393)  /rpt_family="AluSq"  No.:  No.:  7.21e-55  Length: 147021  It Similarity: 55.06% Conservative: 36  Patches: 176  Conservative: 36  Match: 35.01% Mismatches: 98  Match: 95  Match: 1645.71% Mismatches: 98  Mismatches: 16  Mismat	/rpt_family="Alusq"  No.:  7.21e-55  Length: 147021  it Similarity: 55.06% Conservative: 36 Conservative: 36 Match: 98 Match: 95.81% Mismatches: 98 Match: 95.81% Mismatches: 75 Gaps: 11  077-111-13 (1-384) x AC006501 (1-147021)  1 MetvallysLeuileHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20 106573 ATGGTGAAACTGATTCACACATTAGCTGATCATGGTGACAACTGCTGTGCCTTTC 106514  21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrlleArgLeuTyrSerLeuArg 40 106513 TCCTTTTCCCTCTTGGCTACTTGCTCCTTGGACAAAACAATTCGCCTGTTACGT 106454  41 AspPheThrGluLeuProchess	repeat_region
Complement (6014860393)  /**TPt_family="Alusq"**  No.:  No.:  7.21e-55  Length: 147021  Restratty: 55.06* Conservative: 36 Conservative: 36 Matches: 98 Match: 98 Match: 99  O77-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaphe 20  106573 ATGGTGAAACTGATTCACACATTAGCTGATCATCATGGTGACGATGTCAACTGCTTCCTTC	/rpt_family="AlluSq"  nent Scores:  NO.:  7.21e-55  Length: 147021  15 Similarity: 55.06%	repeat_region
Complement (6014860393)  // rpt_family="Alusq"	/rpt_family="AluSq"  ment Scores:  No.:  1.	repeat_region
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Complement (6014860393)  /rpt_family="Alusq"  No.:  No.:  7.21e-55  Length: 147021  It Similarity: 55.06% Conservative: 36 Conservative: 36 Conservative: 36 Match: 35.81% Mismatches: 98 Match: 75  O77-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeulleHisThricuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20 106573 ATGGTGAAACTCACTTACCTATTACCTGATCACACTTGCTGACCATTCCCTTC 106514	/rpt_family="AluSq"  nent Scores:  No.:  7.21e-55  Length: 147021  16 Similarity: 733.00 Matches: 176 Conservative: 36 Match: 98 Match: 95.06%  Conservative: 98 Match: 95.81% Indels: 75 Gaps: 11  077-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20 106573 ATGGTGAAACTGATTCACACATTAGCTGATCACAGTGAACGATGTCAACTGCTTCCTTC	repeat_region complement (60148 .60393)  /rpt_family="AluSq"  nent Scores:  No.:  7.21e-55 Length: 147021  16 Similarity: 55.06% Conservative: 36 Mismatches: 98 Match: 95.81% Indels: 75  O77-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeuIleHsThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20 106573 ATGGTGAAACTGATTCACACATTAGCTGATCATGGTGACGATGTCAACTGTTGGCTCTTC 106514  21 SerPheSerLeuLeuAlaThrCysSerLeuAspLysThrIleArgLeuTyrSerLeuArg 40 106513 TCCTTTTCCCTCTGGCTACTTGCTCTGGCTACAAAAACAATTCGCTGTACCTTCGTTACGT 106454  41 AspPheThrGluLeuProHisSerProLeuLysPheHisThrTyrAlaValHisCysCys 60
Complement (6014860393)  /rpt_family="Alusq"  No.:  No.:  7.21e-55  Length: 147021  It Similarity: 55.06% Conservative: 36  Matches: 98 Ascoal Similarity: 45.71% Mismatches: 98 Match: 95 Match: 95  O77-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeuIleHisThricuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 20  106573 ATGGTGAAACTGATTCACACATTAGCTGATCATCATGGTGACGATGTCAACTGCTTCCTTC	/rpt_family="AluSq"  nent Scores:  No.:  7.21e-55  Length:  733.00  Matches:  733.00  Matches:  16  Conservative:  36  Match:  35.01%  Mismatches:  98  Match:  98  Match:  17  1077-111-13 (1-384) x AC006501 (1-147021)  1 MetValLysLeulleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaphe  1 MetValLysLeulleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaphe  1 MetValLysLeulleHisThrCysSerLeuAspCysThrIleArgLeuTyrSerLeuArg  1	repeat_region complement (60148 .60393)  /rpt_family="Alusq"  nent Scores:  No.:  7.21e-55
Complement (6014860393)  /**TPt_family="Alusq"** No.: No.: No.: No.: No.: No.: No.: No.:	/rpt_family="AluSq"  ment Scores:  No.:  1.	repeat_region complement (60148 .60393)  /rpt_family="Alusq"  nent Scores: No.: 1.21e-55
Complement (6014860393)  /*FPt_family="AluSq"  ment Scores: No.: No.: No.: No.: No.: No.: No.: No.	/rpt_family="AlluSq"  ment Scores:  No.:  7.21e-55  Length: 147021  it Similarity: 55.06% Conservative: 98 Match: 95.81% Indels: 977-111-13 (1-384) x AC006501 (1-147021)  1 MetvallysLeuIleHisThrLeuAlaAspHisGlyAspAspValAsnCysCysAlaPhe 106573 ATGGTGAAACTGATTCACACATTAGCTGATCATACTGTGACGATTCAACTGCTTC 106514	repeat_region complement (60148 .60393)  /rpt_family="Alusq"  No.: 7.21e-55

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105619	368	105679	348	105711	328	105712	308	105739	288	105799	272
105619 TCTTAAAATTAAG 105607	368 nArgThrLeuLys 372	105679 AGGTCAAAAACCCAGAGAGTTGTTTAATATGATTCTTATAGTAGATTTCTTATAGTAGATTTCTTATAGTAGATTTCTTATAGTAGATTTCTTATAGTAGATTTCTTATAGTAGATTTCTTATAGTAGATTTCTTATAGTAGATTTCTTTATAGTAGATTCTTTAGTAGATTCTTTAGTAGATTCTTTAGTAGATTTCTTTAGTAGATTCTTTAGTAGATTCTTTAGTAGATTCTTTAGTAGATTCTTTAGTAGTAGATTCTTTAGTAGATTCTTTAGTAGATTCTTTAGTAGATTCTTTAGATTCTTTAGTAGATTCTTTAGTAGATTCTTTAGTAGATTCTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTTAGATTCTTAGATTCTTAGATTCTTAGATTCTTTAGATTCTTAG	SLYSLYSARGThrSerPrometThragmI control IIIIIITAACTGGCCTTCTAA 105680	5711	oValIleAlaSerAspGlyTyrSerTyrGl;[VsGl;]	328 328	308 uSerSerGlyIleProAspGluPheIleCysProTlembar 10571:	GGGTGACAGA	uGlyLeuArgSerLvsVallanararicallanaricACACCACTGTACTCCAGCCT 10574	105799 ACGTGAACCCAGGAGGCGGAGCTTGCAGTGACGCCAGGAGCTTGCAGTGAACCCCAGGAGGCGGAGCTTGCAGTGACGCCAGGAGCTTGCAGTGAACGCCAGGAGGCGGAGCTTGCAGTGAACGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	LeuAsnLeuThrLysGluSerLenala

AC096419

245795 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-24D13, WORKING DRAFT SEQUENCE.
AC096419.6 GI:30520867
HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_FULLTOP..
Rattus norvegicus (Norway rat)
Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Baden, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barastead, M., Benahmed, F., Blark, D., Barber, M., Barnstead, M., Benahmed, F., Cardenas, V., Carter, K., Cavazos, I., Cessar, H., Center, A., Cardenas, V., Carter, K., Eyrant, R., Chen, Y., Chen, Z., Chu, J., Chavez, D., Chen, B., Even, M., Cree, A., D'Souza, I., Claveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, I., Dayla, C., Dayla, R., Dayla, C., Derano, S., Dumn, A., Durbin, K., Duval, B., Baves, K., Egan, A., Egcotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Gabisi, A., Garta, R., Garcia, A., Garrer, T., Garza, M., Garrer, F., Hadland, W., Hamil, C., Hamilton, C., Liu, J., Jacob, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Mackeon, A., Martin, R., Martinez, B., Parke, K., Parke, M., Perez, A., Perez, L., Pfannkoch, C., Parke, K., Pondexter, A., Popovic, D., Prankoch, C., Parke, K., Pondexter, A., Popovic, D., Pfannkoch, C., Parke, K., Pondexter, L., Parke, K., Parke, K., Pondexter, L., Parke, K., Parke,

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